Claims

1. A device for the isolation and/or purification of nucleic acid molecules comprising at least two layers, a first layer being adapted to bind and/or inactivate inhibitors of the activity of reagents or enzymes used in nucleic acid manipulation and a second layer being adapted to separate a plurality of nucleic acid molecules with respect to their size.

2. The device of claim 1, wherein said first layer is arranged above the second layer.

3. The device of claim 1 or 2, wherein said first layer is a first phase of a gel and said second layer is a second phase of said gel.

4. The device of claim 3, wherein said gel is an agarose-gel or a polyacrylamid-gel.

5. The device of any one of claims 1 to 4, wherein said first layer comprises polyvinylpyrrolidone (PVP), polyvinylpolypyrrolidone (PVPP), CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, antibodies, aptamers, lectins, nucleic acids or ion-exchanger.

6. The device of any one of claims 1 to 5, wherein said second layer is substantially free of PVP, PVPP, CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, aptamers, antibodies, lectins, nucleic acids or ion-exchanger.

7. The device of any one of claims 3 to 6, wherein the device is electrically biased to enhance flow of (a) sample(s) through the layers.

8. The device of any one of claims 3 to 7, wherein said first layer comprises sample loading means.

9. The device of claim 8, wherein said loading means are provided in an array in an upper portion of the first layer, defining an array of columns, each being capable of isolating nucleic acid molecules.

10. The device of any one of claims 1, 5, 6, 7, 8 or 9, wherein said first layer is arranged below the second layer.

11. The device of claim 10, which is a column comprising said first and said second layer.

12. The device of claim 10 or 11, wherein said second layer is a first phase of a column and said first layer is a second phase of said column.

13. The device of any one of claims 10 to 12, said first layer is a matrix comprising PVP, PVPP, CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, aptamers, antibodies, lectins, nucleic acids or ion-exchanger.

14. The device of any one of claims 10 to 13, wherein said second layer is a matrix which is substantially free of PVPP PVP, PVPP, CTAB, EDTA, EGTA, cyclodextrins, proteins, (poly)peptides, aptamers, antibodies, lectins, nucleic acids or ion-exchanger.

15. The device of claims 13 or 14, wherein said matrix of said first and/or second layer is selected from the group consisting of agarose, sepharose™, sephadex™, sephacryl™, BioGel™, superose™ and acrylamid.

16. The device of any one of claims 1 to 15, wherein said nucleic acid molecule is DNA or RNA.

17. The device of claim 16, wherein said DNA is genomic DNA.

18. The device of claim 16 or 17, wherein said nucleic acid molecule is derived from (micro)organisms of soil, sediments, water or symbiotic/parasitic

consortia.

19. The device of claim 18, wherein said (micro)organisms are (micro)organisms of aquatic plancton, microbial mats, clusters, sludge flocs, or biofilms.

20. The device of claim 18 or 19, wherein said (micro)organism are isolated as consortia of coexisting species.

21. The device of any one of claims 1 to 20, wherein said nucleic acid molecules represent a fraction of the metagenome of a given habitat.

22. A method for the isolation of a nucleic acid molecule comprising applying a sample to the device as defined in any one of claims 1 to 21.

23. The method of claim 22, wherein a fraction of the metagenome is isolated from a given habitat.

24. A method for the generation of at least one gene library, comprising the steps of
    (a) isolating and/or purifying nucleic acid molecules from a sample using a device as defined in any one of claims 1 to 21 and optionally amplifying said nucleic acid molecules;
    (b) cloning the isolated and/or purified and optionally amplified nucleic acid molecules into appropriate vectors; and
    (c) transforming suitable hosts with said suitable vectors.

25. The method of claim 24, wherein said suitable hosts are selected from the group consisting of E. coli, Pseudomonas sp., Bacillus sp, Streptomyces sp, other actinomycetes, myxobacteria, yeasts and filamentous fungi.

26. A gene library obtained by the method of claim 24 or 25.

27. A gene library generated from metagenomic nucleic acid molecules from non-

planctonic (micro)organisms comprising average insert sizes of at least 50 kB, of at least 55 kB, of at least 60 kB, of at least 80 kB, of at least 90 kB or of at least 100 kB.

28. A gene library generated from metagenomic nucleic acid molecules from planctonic (micro)organisms comprising average insert sizes of at least 85 kB, at least 90 kB, at least 95 kB, at least 100 kB, at least 120 kB, at least 140 kB, at least 160 kB or at least 200 kB.

29. A nucleic acid molecule comprising a DNA as depicted in SEQ ID NO: 1 or a DNA as deposited under EMBL accession number A3496176.

30. A nucleic acid molecule representing a part of the genome of a non-thermophilic crenarchaeota, whereby said nucleic acid molecule has at least one of the following features:

(a) it contains at least one ORF which encodes a polypeptide having the amino acid sequence SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35;

(b) comprises the DNA sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34;

(c) it comprises portion of at least 20 nucleotides, preferably 100 nucleotides, more preferably at least 500 nucleotides which hybridise under stringent conditions to the complementary strand of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34;

(d) it is degenerate as a result of the genetic code with respect to the nucleic acid molecule of (c); or

(e) it is at least 50% identical with the nucleic acid molecule of SEQ ID NO: 2, SEQ ID NO: 20 or SEQ ID NO: 30, 45% identical with the nucleic acid molecule of SEQ ID NO: 8 or SEQ ID NO: 26, 35% identical with the nucleic acid molecule of SEQ ID NO: 16, SEQ ID NO: 22 or SEQ ID NO: 24 or 30% identical with the nucleic acid molecule of SEQ ID NO: 4, SEQ ID NO: 14, SEQ ID NO: 18 or SEQ ID NO: 28;

31. The nucleic acid molecule of claim 29 or 30, which is DNA or RNA.

32. A vector comprising the nucleotide acid molecule of any one of claims 29 to 31.

33. A host transfected or transformed with the vector of claim 32.

34. A method for producing a (poly)peptide as encoded by a nucleic acid molecule of any one of claims 29 to 31, comprising culturing the host of claim 33 under suitable conditions and isolating said polypeptide from the culture.

35. A (poly)peptide encoded by a nucleic acid molecule of any one of claims 29 to 31 or as obtained by the method of claim 34.

36. The (poly)peptide of claim 35 which is glycosylated, phosphorylated, amidated and/or myristylated.

37. An antibody or an aptamer specifically recognizing the (poly)peptide of claim 35 or 36 or a fragment or epitope thereof.

38. The antibody of claim 37, which is a monoclonal antibody.

39. A transgenic non-human mammal whose somatic and germ cells comprise at least one gene encoding a functional polypeptide selected from the group

consisting of:

(a) the polypeptide of claim 35 or 36;

(b) a polypeptide having an amino acid sequence that is at least 60%, preferably at least 80%, especially at least 90%, advantageously at least 99% identical to the amino acid sequence of (a); and

(c) a polypeptide having the amino acid sequence of (a) with at least one conservative amino acid substitution.